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F1632 H/10  
10-30-01  
PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,712A

DATE: 07/05/2001

TIME: 10:42:51

Input Set : A:\37157SEQ.txt

Output Set : N:\CRF3\07052001\I763712A.raw

OCT 12 2001

TECH CENTER 1600/2900

ENTERED

3 <110> APPLICANT: Wakamiya, N.  
5 <120> TITLE OF INVENTION: Novel Collectin  
7 <130> FILE REFERENCE: 19036/37157  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/763,712A  
C--> 9 <141> CURRENT FILING DATE: 2001-05-04  
9 <150> PRIOR APPLICATION NUMBER: JP HEI 10-237611  
10 <151> PRIOR FILING DATE: 1998-08-24  
12 <160> NUMBER OF SEQ ID NOS: 32  
14 <210> SEQ ID NO: 1  
15 <211> LENGTH: 2024  
16 <212> TYPE: DNA  
17 <213> ORGANISM: Homo Sapiens  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (670)..(1695)  
23 <400> SEQUENCE: 1  
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25 tctcataatg tggatcatcat gaacctcaac aacctgaacc tgacctcaggt gcagcagag 120  
26 aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc 180  
27 aagaacgact ttcaaaatct gcagcaggtt tttcttcaag ccaagaagga cacggattgg 240  
28 ctgaaggaga aagtgcagag ctgagcagag ctggctgcca acaactctgc gttggccaaa 300  
29 gccacaacg acacctgga ggatataaac agccagctca actcattcac aggtcagatg 360  
30 gagaacatca ccactatctc tcaagccaac gaggagaacc tgaaagacct gcaggactta 420  
31 cacaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag 480  
32 ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg 540  
33 cggacgctga ccagcaatct aatgaagtc aggaccactt gcacagatac ccttaccaaa 600  
34 cacacagatg atctgaacct cttgaataat accctggcca acatccgttt ggattctgtt 660  
35 tctctcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta 711  
36 Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val  
37 1 5 10  
38 gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag 759  
39 Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys  
40 15 20 25 30  
41 cat ggt cag ctg atc aag aat ttt aca ata cta caa ggt cca ccg ggc 807  
42 His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly  
43 35 40 45  
44 ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca 855  
45 Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro  
46 50 55 60  
47 act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct 903  
48 Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro  
49 65 70 75  
50 ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga 951  
51 Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly  
52 80 85 90  
53 gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc 999  
54 Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser

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1047

55	95		100		105		110	
56	cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca							
57	Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro							
58		115		120		125		
59	ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc						1095	
60	Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly							
61		130		135		140		
62	cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg						1143	
63	Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val							
64		145		150		155		
65	cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca						1191	
66	Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro							
67		160		165		170		
68	ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg						1239	
69	Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val							
70	175		180		185		190	
71	ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc						1287	
72	Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly							
73		195		200		205		
74	tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca						1335	
75	Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser							
76		210		215		220		
77	gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag						1383	
78	Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys							
79		225		230		235		
80	tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata						1431	
81	Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile							
82		240		245		250		
83	aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac						1479	
84	Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp							
85	255		260		265		270	
86	tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac						1527	
87	Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp							
88		275		280		285		
89	tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat						1575	
90	Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His							
91		290		295		300		
92	ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac						1623	
93	Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn							
94		305		310		315		
95	gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg						1671	
96	Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg							
97		320		325		330		
98	gag aca gta ctg tca tct gca tta taacggactg tgatgggatc acatgagcaa						1725	
99	Glu Thr Val Leu Ser Ser Ala Leu							
100	335		340					
101	attttcagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcatcagat						1785	
102	tgaaaaaaaaaaa aaagcactg aaaaccaatt actgaaaaaaaa aattgacagc tagtggtttt						1845	
103	taccatccgt cattacccaa agacttggga actaaaatgt tccccagggt gatatgctga						1905	

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104 ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965

105 atacaaatta tgtcttccaa agtatggaac actccaatca gaaaaagggtt atcatcccg 2024

107 &lt;210&gt; SEQ ID NO: 2

108 &lt;211&gt; LENGTH: 547

109 &lt;212&gt; TYPE: PRT

110 &lt;213&gt; ORGANISM: Homo Sapiens

112 &lt;220&gt; FEATURE:

113 &lt;223&gt; OTHER INFORMATION: Deduced Amino Acid Sequence of Novel Collectin from

## Nucleotide

114 Sequence

116 &lt;400&gt; SEQUENCE: 2

117 Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu

118 1 5 10 15

119 Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val

120 20 25 30

121 Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn

122 35 40 45

123 Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys

124 50 55 60

125 Glu Lys Val Gln Ser Leu Gln Thr Leu Ala Ala Asn Asn Ser Ala Leu

126 65 70 75 80

127 Ala Lys Ala Asn Asn Asp Thr Leu Glu Asp Met Asn Ser Gln Leu Asn

128 85 90 95

129 Ser Phe Thr Gly Gln Met Glu Asn Ile Thr Thr Ile Ser Gln Ala Asn

130 100 105 110

131 Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu His Lys Asp Ala Glu Asn

132 115 120 125

133 Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu Glu Arg Phe Gln Leu Phe

134 130 135 140

135 Glu Thr Asp Ile Val Asn Ile Ile Ser Asn Ile Ser Tyr Thr Ala His

136 145 150 155 160

137 His Leu Arg Thr Leu Thr Ser Asn Leu Asn Glu Val Arg Thr Thr Cys

138 165 170 175

139 Thr Asp Thr Leu Thr Lys His Thr Asp Asp Leu Thr Ser Leu Asn Asn

140 180 185 190

141 Thr Leu Ala Asn Ile Arg Leu Asp Ser Val Ser Leu Arg Met Gln Gln

142 195 200 205

143 Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val Ala Asn Leu Ser Val

144 210 215 220

145 Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys His Gly Gln Leu Ile

146 225 230 235 240

147 Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly Pro Arg Gly Pro Arg

148 245 250 255

149 Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro Thr Gly Asn Lys Gly

150 260 265 270

151 Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Glu

152 275 280 285

153 Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly Gly Lys

154 290 295 300

155 Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser Arg Gly Ser Pro Gly

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```

156 305          310          315          320
157 Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro Gly Pro Pro Gly Pro
158          325          330          335
159 Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln
160          340          345          350
161 Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly
162          355          360          365
163 Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro
164          370          375          380
165 Pro Gly Pro Pro Gly Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln
166 385          390          395          400
167 Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly Cys Pro Pro His Trp
168          405          410          415
169 Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile
170          420          425          430
171 Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val
172          435          440          445
173 Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val
174          450          455          460
175 Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn
176 465          470          475          480
177 Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys
178          485          490          495
179 Ala Gly Gln Pro Asp Asn Trp Gly His Gly His Gly Pro Gly Glu Asp
180          500          505          510
181 Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu
182          515          520          525
183 Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser
184          530          535          540
185 Ser Ala Leu
186 545

```

188 &lt;210&gt; SEQ ID NO: 3

189 &lt;211&gt; LENGTH: 27

190 &lt;212&gt; TYPE: PRT

191 &lt;213&gt; ORGANISM: Artificial Sequence

193 &lt;220&gt; FEATURE:

194 <223> OTHER INFORMATION: Modified Consensus Sequence of collectins Hybridizable with Novel

195 Collectin

197 &lt;400&gt; SEQUENCE: 3

198 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn

199 1 5 10 15

200 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe

201 20 25

203 &lt;210&gt; SEQ ID NO: 4

204 &lt;211&gt; LENGTH: 21

205 &lt;212&gt; TYPE: DNA

206 &lt;213&gt; ORGANISM: Artificial Sequence

208 &lt;220&gt; FEATURE:

209 <223> OTHER INFORMATION: Sequence of a Reverse Primer for Screening a Novel Collectin.

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211 <400> SEQUENCE: 4  
 212 caatctgatg agaaggtgat g 21  
 214 <210> SEQ ID NO: 5  
 215 <211> LENGTH: 21  
 216 <212> TYPE: DNA  
 217 <213> ORGANISM: Artificial Sequence  
 219 <220> FEATURE:  
 220 <223> OTHER INFORMATION: Sequence of a Forward Primer for Screening a Novel  
 Collectin.  
 222 <400> SEQUENCE: 5  
 223 acgaggggct ggatgggaca t 21  
 225 <210> SEQ ID NO: 6  
 226 <211> LENGTH: 27  
 227 <212> TYPE: PRT  
 228 <213> ORGANISM: Artificial Sequence  
 230 <220> FEATURE:  
 231 <223> OTHER INFORMATION: Consensus sequence of three collectins which were reported  
 232 heretofore  
 234 <400> SEQUENCE: 6  
 235 Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro  
 236 1 5 10 15  
 237 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe  
 238 20 25  
 240 <210> SEQ ID NO: 7  
 241 <211> LENGTH: 24  
 242 <212> TYPE: DNA  
 243 <213> ORGANISM: Artificial Sequence  
 245 <220> FEATURE:  
 246 <223> OTHER INFORMATION: M13 Universal Primer Sequence for Sequencing  
 248 <400> SEQUENCE: 7  
 249 cgacgttgta aaacgacggc cagt 24  
 251 <210> SEQ ID NO: 8  
 252 <211> LENGTH: 17  
 253 <212> TYPE: DNA  
 254 <213> ORGANISM: Artificial Sequence  
 256 <220> FEATURE:  
 257 <223> OTHER INFORMATION: M13 Reverse Primer Sequence for Sequencing.  
 259 <400> SEQUENCE: 8  
 260 caggaaaca gctatgac 17  
 262 <210> SEQ ID NO: 9  
 263 <211> LENGTH: 24  
 264 <212> TYPE: DNA  
 265 <213> ORGANISM: Artificial Sequence  
 267 <220> FEATURE:  
 268 <223> OTHER INFORMATION: Sequence of a lambda gtl1 Reverse Primer for Sequencing.  
 270 <400> SEQUENCE: 9  
 271 ttgacaccag accaactggt aatg 24  
 273 <210> SEQ ID NO: 10  
 274 <211> LENGTH: 24  
 275 <212> TYPE: DNA

VERIFICATION SUMMARY

DATE: 07/05/2001

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Input Set : A:\37157SEQ.txt

Output Set: N:\CRF3\07052001\I763712A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date